



Docket No.: CL000685

Serial No.: 09/748,127

Inventors: YAN, Chunhua et al.

Title: ISOLATED HUMAN DRUG-METABOLIZING...

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1 TTTCTTCTGT TTGCTTACTC CCTATCCGGG GGCCCAAGGC GCTGTCTCCG
51 CCGCCCAAGC CCCGCGTAAA CCTGGGTGAC CTCGGAGACA TCCGTTGGAG
101 CATGAGTTCC CGACATCAGG CGGCGGCGGT GGTCCGGGAG AAACCCGGCG
151 GCGGGGAGAT AAGCCTGCCC AGGAGGCAGG GGGCTGGGCT AGCTGCCCCG
201 CCCC CGCCT GACTTCGTTG GGGAGGGAGA CGCCCGGCTC CCGCCCTTAA
251 CTAGCCAGC CGCGCGGAGC GCCTGGGAGA GGAGAAGGAG CCGACCTGCC
301 GAGATGGAGG CGACCGGCAC CTGGGCGCTG CTGCTGGCGC TGGCGCTGCT
351 CCTGCTGCTG ACGCTGGCGC TGTCGGGAC CAGGGCCCGA GGCCACCTGC
401 CCCC CGGCGC CACGCCGCTA CCACTGCTGG GAAACCTCCT GCAGCTACGG
451 CCCC CGGCGC TGTAATCAGG GCTCATGCGG CTGAGTAAGA AGTACGGACC
501 GGTGTTTACC ATCTACCTGG GACCTGCGG GCCTGTGGTG GTCTGTGTTG
551 GGCAGGAGGC TGTGCGGGAG GCCCTGGGAG GTCAGGCTGA GGAGTTCAGC
601 GGCCCGGGAA CCGTAGCGAT GCTGGAAGGG ACTTTTGATG GCCATGGGGT
651 TTTCTTCTCC AACGGGGAGC GGTGGAGGCA GCTGAGGAAG TTTACCATGC
701 TTGCTCTGCG GGACCTGGGC ATGGGGAAGC GAGAAGGCGA GGAGCTGATC
751 CAGGCGGGAG CCGGTGTCTT GGTGGAGACA TTCAGGGGA CAGAAGGACG
801 CCCATTGATG CCCTCCCTGC TGCTGGCCCA GGCCACCTCC AACGTAGTCT
851 GCTCCCTCCT CTTTGGCCTC CGCTTCTCCT ATGAGGATAA GGAGTTCAGC
901 GCCGTGGTCC GGGCAGCTGG TGGTACCTCG CTGGGAGTCA GCTCCAGGGG
951 GGGTCAGACC TACGAGATGT TCTCTGGTT CCTGCGGCC CTGCCAGGCC
1001 CCCACAAGCA GCTCCTCCAC CACGTCAGCA CCTTGGCTGC CTTTCAAGTC
1051 CCGCAGGTGC AGCAGCACCA GGGGAACCTG GATGCTTCGG GCCCCGACG
1101 TGACCTTGTC GATGCTTCC TGCTGAAGAT GGCACAGGAG GAACAAAACC
1151 CAGGCACAGA ATTCACCAAC AAGAATATGC TGATGACAGT CATTTATTTG
1201 CTGTTTGTCT GGACGATGAC GGTGAGCACC ACGGTCGGCT ATACCTCCT
1251 GCTCCTGATG AAATACCTC ATGTCCAAA GTGGGTACGT GAGGAGCTGA
1301 ATCGGGAGCT GGGGCTGGC CAGGCACCA GCCTAGGGGA CCGTACCCGC
1351 TCTCCTTACA CCGACGCGGT TCTGCATGAG GCGCAGCGGC TGCTGGCGCT
1401 GGTGCCCATG GGAATACCCC GCACCCTCAT GCGGACCACC CGCTTCCGAG
1451 GGTACACCTT GCCCAGGGC ACGGAGGTCT TCCCCCTCCT TGGCTCCATC
1501 CTGCATGACA CCAACATCTT CAAGCACCCA GAAGAGTTCA ACCCAGACC
1551 TTTCTGGAT GCAGATGGAC GGTTCAGGAA GCATGAGGCG TTTCTGCCCT
1601 TCTCCTTAGG GAAGCGTGTG TGCTTGGAG AGGGCTGGC AAAAGCGGAG
1651 CTCTTCTCTT TCTTACCAC CATCCTACAA GCCTTCTCCC TGGAGAGCCC
1701 GTGCCGCGCG GACACCTGA GCCTCAAGCC CACCGTCAGT GGCCTTTTCA
1751 ACATTCCCCC AGCCTTCCAG CTGCAAGTCC GTCCCACTGA CTTTCACTCC
1801 ACCACGAGA CAGATGAAG GAAGGCAACT TGGAGTGGT GGGTGCCAG
1851 GACGTGCGCT CCAGCTCAA CAGTGGGAT GGACAGGTT AATGTCTCCA
1901 GAGTGATAC TGCAAGCAGC CACATTTACA CGCTGCACTG CTAAGATGCA
1951 AGTCTGTCCC ACGGCCACA CGCTCACTTG ACTCATGCTG CTAAGATGCA
2001 CAACCGCACA CCCATACACA ACTACAAGGG CCACAAAGCA ACTGCTGGGT
2051 TAGCTTTCCA CAGACATAA TATAGTCCAT CTGCAATCAC AAGCACATAG
2101 CCAGGTAACC CACCAACTCC CTTGGATCTG CAGCCACAC GTGGGAGTCT
2151 GGCTGTACCC TTCAACAAGC ACAGAAACGG CCACACATGT TCACAGCTCA
2201 CACGCCCTCT CCATTATCG AACTTCTCAG TGTCCCTGTC CCTGGTGCCT
2251 GGCACAGGGA ACAGCATGCC CCCTCCGGGG TCATGCCACC CAGAGACTGT
2301 CGCTGTCTAT GGCCTCACT CATGCTCCCT CTCTTGGCTA CACCACTCTC
2351 CCAGCCTGTG ACCACCGATG TCCACACACC CCCAACCACT TGTCCACACA
2401 GCTACCCACG TACGACATCG TCCTGGCTCC CCAGAGTATC TTCCCACTGA
2451 GACACGCGCG CCCACAGAG GCACAGTCCC CAGCCACCTC TGCAACTGCA
2501 GCCCTCAGT ACCCTTTTTT AAGCACCTG ATTCTACCA ATGCAAAAC
2551 ATCTGGGTCT GCGATTATGC ACAGAGACTT TGGACATACG AGGACCTCA
2601 GACCGGAGGA ACACCTGCC AACCCTAACA CGTGCTTATG TAACCACGTG
2651 GAAAGCGGCC CCTGCTGCC CTCCACACAC ACATACACAC TCACTGATCT
2701 ACAGCCCTGT TCGGCGTCA GAGTCCCAAC TAGACCCAGT GGAAGGGGTT
2751 AGAGACCAAG TAGGGGCCAG TTTCCAATTC ACCCTGTGAG GGAGTGAGCC
2801 GGATCTGACG TTCCTGTGA CTTAAGGGTC CGGCTTGGGA ATTAAGTTT
2851 GTTCTGGCC TTTAGCCTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2901 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA (SEQ ID NO:1)
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FEATURES:

5'UTR: 1-303

Start Codon: 304

Stop Codon: 1815

3'UTR: 1818

FIGURE 1A



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HOMOLOGOUS PROTEINS:

gi 117254 sp P24461 CPG1_RABIT CYTOCHROME P450 2G1 (CYP1IG1) (P...	516	e-145
gi 404777 gb AAA31432.1 (L10912) cytochrome P-450 2B-Bx [Oryct...	513	e-144
gi 479930 pir S35666 cytochrome P450 2B4 isoform Bx - rabbit >...	513	e-144
gi 117212 sp P00178 CPB4_RABIT CYTOCHROME P450 2B4 (CYP1IB4) (P...	508	e-143
gi 320075 pir S31277 cytochrome P450 2B4-B1 - rabbit >gi 21369...	508	e-143
gi 4731350 gb AAD28466.1 (AF128849) cytochrome P450 2B10 relat...	508	e-143
gi 3123191 sp P04167 CPB2_RAT CYTOCHROME P450 2B2 (CYP1IB2) (P4...	508	e-143
gi 117213 sp P12789 CPB5_RABIT CYTOCHROME P450 2B5 (CYP1IB5) (P...	507	e-142
gi 89973 pir A27717 cytochrome P450 2B5, hepatic (form HP1) - ...	507	e-142
gi 2144292 pir O4RTP2 cytochrome P450 2B2 - rat	506	e-142

EST:

gb BE148597 BE148597 MR0-HT0241-150500-010-b02 HT0241 Homo sapi...	1091	0.0
gb BF359243 BF359243 RC6-ET0072-150600-011-F01 ET0072 Homo sapi...	779	0.0
gb AW753778 AW753778 RC1-CT0286-301099-011-f08 CT0286 Homo sapi...	652	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:

gb BE148597	head_neck
gb BF359243	lung_tumor
gb AW753778	colon

Tissue expression:
Human leukocyte

FIGURE 1B



1 MEATGTWALL LALALLLLLT LALSGTRARG HLPPGPTPLP LLGNLLQLRP
51 GALYSGLMRL SKKYGPVFTI YLGPWRPVVV LVGQEAVREA LGGQAEFSG
101 RGTVAMLEGT FDGHGVFFSN GERWRQLRKF TMLALRDLGM GKREGEELIQ
151 AEARCLVETF QGTEGRPFDP SLLLAQATSN VVCSLLFGLR FSYEDKEFQA
201 VVRAAGTLL GVSSQGGQTY EMFSWFLRPL PGPHKQLLHH VSTLAAFTVR
251 QVQHQGNLD ASGPARDLVD AFLKMAQEE QNPGTEFTNK NMLMTVIYLL
301 FAGTMTVSTT VGYTLILLMK YPHVQKWVRE ELNRELGAGQ APSLGDRTRL
351 PYTDAVLHEA QRLALVPMG IPRTLMTTR FRGYTLPQGT EVFPLLGSIL
401 HDPNIFKHPE EFNPDRLDA DGRFRKHEAF LPFSLGKRVC LGEGLAKAEL
451 FLFFTTILQA FSLESPCPPD TLSLKPTVSG LFNIPPAFQL QVRPTDLHST
501 TQTR (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

Prosite search results:

[1] PDOC00004 PS00004 CAMP_PHOSPHO_SITE

CAMP- and cGMP-dependent protein kinase phosphorylation site

128-131 RKFT

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE

Protein kinase C phosphorylation site

Number of matches: 6

1 61-63 SKK
2 99-101 SGR
3 248-250 TVR
4 288-290 TNK
5 378-380 TTR
6 473-475 SLK

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE

Casein kinase II phosphorylation site

Number of matches: 3

1 119-122 SNGE
2 192-195 SYED
3 343-346 SLGD

[4] PDOC00008 PS00008 MYRISTYL

N-myristoylation site

Number of matches: 10

1 51-56 GALYSG
2 109-114 GTFDGH
3 115-120 GVFFSN
4 188-193 GLRFSY
5 207-212 GTLLGV
6 257-262 GNLDAS
7 284-289 GTEFTN
8 339-344 GQAPSL
9 370-375 GIPRTL
10 444-449 GLAKAE

[5] PDOC00009 PS00009 AMIDATION

Amidation site

Number of matches: 2

1 140-143 MGKR
2 435-438 LGKR

[6] PDOC00029 PS00029 LEUCINE_ZIPPER

Leucine zipper pattern

Number of matches: 2

1 32-53 LPPGPTPLPLGNLLQLRPGAL
2 39-60 LPLGNLLQLRPGALYSGLMRL



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[7] PDOC00081 PS00086 CYTOCHROME_P450
Cytochrome P450 cysteine heme-iron ligand signature

433-442 FSLGKRVCLG

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	5	25	2.305	Certain
2	64	84	0.783	Putative
3	170	190	1.041	Certain
4	292	312	2.031	Certain
5	448	468	1.133	Certain

FIGURE 2B



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BLAST Alignment to Top Hit:

>gi|117254|sp|P24461|CPG1_RABIT CYTOCHROME P450 2G1 (CYP11G1)
(P450-NMB) (OLFACTIVE)
pir||B31944 cytochrome P450 2G1 - rabbit
Length = 494

Score = 516 bits (1315), Expect = e-145
Identities = 248/491 (50%), Positives = 345/491 (69%), Gaps = 3/491 (0%)

Query: 1 MEATGTWALLLALAL-LLLLTLALSCTRARGHLPPGPTPLLLGNLLQLRPGALYSGLMR 59
ME G + + LAL LL+ +A + G LPPGPTP+P LGNLLQ+R A + ++
Sbjct: 1 MELGGAFITFLALCFSCLLILIAWKRVQKPGRLPPGPTPIPLGNLLQVVRTDATFQSFLK 60

Query: 60 LSKKYGPVFTIYLGWPWPVVVLVGQEAVERALGGQAEFSGRGTVAMLEGTDFGHGVFFS 119
L +KYGPVFT+Y+GP RPVV+L G EAV+EAL +A+EFSGRG +A +E F GHGV +
Sbjct: 61 LREKYGPVFTVYMG+RPVVILCGHEAVKEALVDRADFEFSGRGELASVERNFQGHGVALA 119

Query: 120 NGERWRQLRKFTMLALRDLGMGKREGELIQAEARCLVETFGTEGRPFDPSSLQAQTS 179
NGERWR LR+F++ LRD GMGKR EE IQ EA L+E F+ T+G P DP+ L++ S
Sbjct: 120 NGERWRILRRFSLTILRDFGMGKRSEIERIQEEAGYLLEFRKTKGAPIDPTFFLSRTVS 179

Query: 180 NVVCSLLFGLRFSYEDKEFQAVVRAAGGTLVGSSQGGQTYEMFSWFLRPLPGPHKQLLH 239
NV+ S++FG RF YEDK+F +++R + + +S+ Q Y+M+S ++ LPG H ++ +
Sbjct: 180 NVISSVVGSRFDYEDKQFLSLLRMINESFIEMSTPWAQLYDMYSGVMQYLPGRHNRYY 239

Query: 240 HVSTLAFTVRQVQHQGNLDASGPARDLVDAFLKMAQEEQNPGTEFTNKNMLMTVIYL 299
+ L F +V+ ++ +LD P RD +D FL+KM Q++ NP TEF KN+++T + L
Sbjct: 240 LIEELKDFIAARVKVNEASLDQNP-RDFIDCFLIKMHQDKNNPHTEFNKLNVLTTNL 298

Query: 300 LFAGTMTVSTTVGYTLLLMKYPHVQKWVREELNRELGAQAPSLGDRTRLPYTDAVLHE 359
FAGT TVS+T+ Y LL+MK+P VQ + EE+N+ +G + PS+ DR ++P+TDAV+HE
Sbjct: 299 FFAGTETVSSTLRYGFLIMKHPEVQTKIYEEINQVIGPHRIPSVDVRVKMPFTDAVIHE 358

Query: 360 AQRLLALVPMGIPRTLMTTRFRGYTLPGQTEVFPLLSILHDPNIFKHPEEFNPDRFLD 419
QRL +VPMG+P ++R T FRGY LP+GT+VFPLLS+L DP F HP++F P FLD
Sbjct: 359 IQRLTDIVPMGVPHNVIRDTHFRGYLLPKGTDVFPPLLSVLKDPKYFCHPDDFYQHFELD 418

Query: 420 ADGRFRKHEAFLPFSLGKRVCLGEGALAEFLFFTTILQAFSLESPPCDTSLKPTVS 479
GRF+K+EAF+PFS GKR+CLGE +A+ ELFL+FT+ILQ FSL PP + + P +S
Sbjct: 419 EQGRFKNEAFVFPSSGKRICLGEAMARMELFLYFTSILQNFSLHPLVPPVNIIDITPKIS 478

Query: 480 GLFNIPPAFQL 490
G NIPP ++L
Sbjct: 479 GFGNIPPTYEL 489 (SEQ ID NO:4)

Hmmer search results (Pfam):

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
PF00067	Cytochrome P450	594.4	6.9e-175	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00067	1/1	33	493 ..	1	497 []	594.4	6.9e-175

FIGURE 2C



1 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
51 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1951 TTGGATCGAA GAGGTCACAG CACCCTCCTC TTTCTTCCTC CTACCCCTGC
2001 GCTGAGTAAG AAGTACGGAC CGGTGTTTAC CATCTACCTG GGACCTTGGC
2051 GGCTGTGGT GGTCTGGTT GGGCAGGAGG CTGTGCGGGA GGCCCTGGGA
2101 GGTGAGGCTG AGGAGTTTCA GGGCCGGGGA ACCGTAGCGA TGCTGGAAGG
2151 GACTTTTGAT GGCCATGGTA AGTCAAGGGC TGCTAGGCCC TCCGCTCACA
2201 GCCTGCCACC ACTTACTGGT GTGTGACCTT TGCACATGGC TTAGTCCCTC
2251 TGTTGCCTCA TCTGTCAAAT GGAGTGATAA CAGTGCCCAT CAGCCGGGTG
2301 CAGTGGCTAG TGCTGAAAT CCAACACTT TGGGAGGCGG AGGTGGGTGG
2351 ATCACTTGAG GTCAGGAGTT CGAGACCAGC CTGGCCAACA TGGTGAAACC
2401 CTGTCTCTAC TAAAAATATA AAAATTAGCT GGGCATGGTG GTGCGTACCT
2451 GTAATCCAG ATACTTGGGA GGTGAGGCA GGAGAATCGC TTGAACCCGG
2501 GAGGCAGATG TTGCAGTGAA CCAAGACTGT GCCACTGCAC TCCAGTCTGG
2551 GCAACAGAGT GAGCCTCCAT CTCAACAAAA CAAACAAAAA GCAGTGCCCA
2601 TCATGTAGGA TTGAGTGATT GAGTGAGGAC TGAGCCTTGT GCAAAGTGAG
2651 CACTCACTAA TCACCAGGTT GTAGTATCAG TGATAACCAT CAATGATCCA
2701 GGTAAAGCCC TGAGGGTTCA GAAAGATGCC GGAGCGCTTT CAAGGTGCTG
2751 GGGATTGGTG GGCAAGCCCT CGAATAATAG AAACAGTTCT CTGTATTACA
2801 ACAGAAAGCA GGAGGCCCAT GCTGGGTGCT GCCAGGAAGT CAGTAGTAAC
2851 TAAGACAGCA CCGGTGCTGC TTCCCAAGCG CACCTAGGCC AGTGGGGAAA
2901 CAGACTCACC ACACAGTCCC AGCCCAAGAGT GGTGAGGGCC AAGATGGGGA
2951 AGCACGGGGA GAAAGGTCAG GGTGGGATGG GGAGGGGTCA GGGCAAGAGG
3001 GGTGAGGGCC AGGCTGAGGG AAGCCCTGGG ACTGTAGGAA TTTAGAGGAG
3051 GTACCTGACC CGGCATGTTT GGTGAGGGAG ATTGAGGAAG TCTTCCTGGA
3101 AGAGAGGCTG TCGGAGCTGA GACTCATAAG ATGAGTGGGG AGGGTGTTC
3151 AGGCAGAAAG ACCAGCACCT ACAAAGCAT GACTTTGAGA GAAGCATTCA
3201 TCCATTCAAC TGATGAATTT TCAGACTGGG CACGTGGCT CATGCTGTA
3251 ATCCAGCAC TTTGGAAGGC TGAATGGGGA GGATGACTTG AGCCTAGGCA
3301 TTTGTGACAA GCCTGGGCAA CATGGTGAGA CCCTGCCTCC AAAAAACAAA
3351 CAAACAAACA AAAAATCATT ATACCTGGTA CCATGGGTAC CAGGTACATA
3401 GAAATGACTC AGGCAGATAT GGTGTCCTCT CCTACTGTGG GAGAGGCGGG
3451 CTTATACTGC AGTAAGACAA TAGAGGGAGG GAATATAATC CTAATAAGAG
3501 AGGTACAGAT TTGAGAGCAA ACACAGGGCA CAGGCATATG TACGAGGGTA
3551 AAGAGGGAAT CAGGGAAGGC TTCTCAGAGA AGGTGACATT TAAGCCGGGA
3601 CATGAAGGAT GAACGAGTTA GTTACCAAG GATGGGATGG AAAGGGGTGA
3651 GAGTGATGGA GGCAGAGGGA ACTGCAGGAT CATAGGCCTA GACAGGGGAT
3701 CCTGACGCC TTGAGGAAGT GAGAGAAGAC CAGCGCAGTC GTAGTGGGTT
3751 AAGTAACAAA GCTGAGAAGC CAGGGAATC CCTGGTCATG CAGGGCTGT
3801 GAGTCACGTC AGAGTGTTTG GGCTTTTGT TTTCTGGGA GCAGTCGATT
3851 TTAAGCAGGG AACAGCTGTA TTCAGAGTTG GGAAGATCCT GTGGTTGCTG

FIGURE 3A



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3901 CCTGAAGGGG ATGAACTGG AGGCTAGGAG CCCAGGGTGA TAGGGAGGAT
3951 CCAGGGTGAT GGGGAGGCTG GGAGGTCCCG GGTGATGGAC CAGGGCTGGG
4001 GCCAGGGGAT GGGGAGGAAG GAGTAATTGG GAGAGGCTG GGGCTCTGGC
4051 CGAGGAATGG ATGGTGGGCT GAAACAGGGA GAGGAGAGAT GCTTAGGCCA
4101 CTTTGGAACA CAGTAGGGCA AGGACAGGAG ACACCCAAGG GGAAGTGCCC
4151 AAGAGACCAC GACAGGCTGG CATTGGACAG GGAAGGTCTG TCTGGAGCAG
4201 GTGTCTTGGG TAAGGGAGGA AAATGGTGCA GTTCCATCCT CCTCCCTCTC
4251 TGTTCACCT CTAAACTACA TGGGGCACAG GACCCAGTGG GACTCCATAA
4301 ATGATGGGAT GGGTGGATGG AAGGAAGGAA GGAGGAAACA ACTCTTCATT
4351 CATCCTGGTT ATTTACAGAA CAGGCCAGGT GCGGTGCTCA CGCTTGCCAT
4401 TCTAGCACTT TGGGAGGCTG AGGTGGGTGG ATTACCTCAG GTCAGGAGTT
4451 CAAGACCAGC CTAGACAACG TAGAGAAACC CCATCTCTAC TGAAGATATA
4501 AAATTAGCTG GGCCTAGTGG CATATGCCTG TAATCCCAGC TAGTCGGGAA
4551 GCTGAGGAGC GAGAATCGCT TGAACCCGAG AGGCAGAGGT TGGGTGAGC
4601 TGAGATCGTG CCATTGCACT CCAGCCTGGG TGACAAAGCA AGACCTCGTC
4651 TCAATAATAA TAATAATTAC AAAACAGAAG GAGCCTGGT CATCCAGCT
4701 ACCTACTTTT CAGGAGAAATG TACTCCCTTA CCCAAGGGCA AAGGATGGGA
4751 GAACCACTTT GATTATGCAT TTATTGAGCA CTTACTGAGT CCTCATCCCT
4801 GGGCTAGGCT GGAATGGACT CAGATGGAGC CTGAAGAGTC CCCCTCAGGG
4851 AACCTCACTA GAAAGAAGGA GGAATCGGCC GGGCGCGGTG GCTCACGCCT
4901 GTAATCCCAA CACTTTGGGA GGCTGAGGTG GGTGGATCAC AAGGTCAGGA
4951 GATCGAGACC ATCCTGGCTA ACACAGTGAA ACCCATCTC TACTAAAAAT
5001 ACAAAAAATG AGCCAGGCAT GGTGGCGGGC GCCTGTAGTC CCAGCTACTC
5051 AGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCGGGAGGCA GAGGTTGCAG
5101 TGAGACGAGA TCACGCCACT GCACTCCAGC CTGGGCAACA GAGCGAGATT
5151 CCGTCTCAAA AAAAAAAGA AAGAAAGGAA GAAGGGGGAA TGGGGGAGAG
5201 GGGCCGGTCC CTTTTTGGT CTAGCCTTCT GCGCAGGGGT TTTCTTCTCC
5251 AACGGGGAGC GGTGGAGGCA GCTGAGGAAG TTTACCATGC TTGCTCTGCG
5301 GGACCTGGGC ATGGGGAAGC GAGAAGGCGA GGAGCTGATC CAGGCGGAGG
5351 CCGGTGTCT GGTGGAGACA TTCCAGGGGA CAGAAGGTCA GCATGGCGGG
5401 GTCACCCAG GGTCTCCAGC CGAGTGAAAG GAAAACTCT CTTACTGTGG
5451 CTGGGGGTGG CCCCACCCA GGTCTGGAA TGGCAGGAG GGAAGCCTT
5501 GAACTCTAGG GCTGGCCTGG GGGTTCTGTT CACTGCCACC TTCTGTCTCT
5551 GTCCCACTGT CTCTCCGAGG CTGTCATGAC ATCTCTCTGT GTGTCTCTGG
5601 TGCTATCATC CCATCTCTCC TGGGTCTCCA TCTCTCTCTC TGTCTCTTTT
5651 CTTTCTCTCT CTTTCTCTCT ATTTTTTGGG CCCTCAGTCT ATCTCTGTTT
5701 CTGTCTCCCT GCTGTGTGA TGGTCACTCT GTTCTTTTCT CCCTGTCTGT
5751 TTCTCTGTCC CTATCTGTCT GTATCCTTCT TTGCCTGTTT AGCTCTCTCC
5801 CTGCGCTGTC CATCCATCTT TCCTGCCTC CCTGTCTCTC TCTGGTTGGG
5851 TTCAGCCCCA ACCTGCTCCC CTCTGCCTGG CTCCATCACA GCCTACCTCC
5901 CTGCCCCCAT TCCCCCAGG ACGCCCATTC GATCCCTCCC TGCTGCTGGC
5951 CCAGGCCACC TCCAACGTAG TCTGCTCCCT CCTCTTTGGC CTCCGCTTCT
6001 CCTATGAGGA TAAGGAGTTC CAGGCCGTGG TCCGGGCAGC TGGTGGTACC
6051 CTGCTGGGAG TCAGCTCCCA GGGGGGTGAG GTGAGTGGGT GGGACCCCTC
6101 TCCAACCTAC TTCCCTGAAG GTTCTGCCA AGGTCCCATG AGAAGTAGTT
6151 GCCCTTCTCC CCACAGACCT ACGAGATGTT CTCCTGGTTC TCGCGGCCCC
6201 TGCCAGGCCC CCACAAGCAG CTCTCCACC ACGTGAGCAC CTTGGCTGCC
6251 TTCACAGTCC GGCAGGTGCA GCAGCACCAG GGGAACTGG ATGCTTCGGG
6301 CCCCAGCAGT GACCTTGTG ATGCTTCTCT GCTGAAGATG GCACAGGTGT
6351 GGGAGGGGTG CAGGGACCCC CTCTCTGAAT GGGCGTGGTG ACCTGGCAGG
6401 TCCCAGCCAG GTGTCCCTGG GGACCTCAAT TGGGTTCCTC TCTCTTTCTC
6451 TCTCTGCATG TCTCTGTGAG TATGAGTGTG TCTGTGCATG TGTGTGCATC
6501 CCTTCTCTGC ACATCTGTGC TGGCCCTTTC AGGGCGTTGC TCTCACTGCC
6551 TCTCCGCCCC CCGACCTGGG CATTTGTGCC GGGCTGTCTG TCTCTCCAGC
6601 ATCTCTCCTC TTTCTCCCTC CCACCTCGGC CCTTGTGTTT AGGCCCCATG
6651 CCCAGGGTCC TACACCAGCA ATCCCCAGGA TCACTTCATC CCATCCCCTG
6701 CAGCTCTCCC AGACTTTTAT GTAATTACAC AATTTTATGT GAATTATGGT
6751 CATTTATTAG GAAGCCTTGC AATATCAAGT TATGTTAATA AAGTCCACTT
6801 TATTAATTAT ATAAGAACA TATTTCTTTT CCTTTTTTTT TTCTTTTCTT
6851 TTTAAAGAGA CAGGATCTCT TTCTGTTGCC CAGGCTAGAG TACAGTTGCA
6901 AAATCATAGC TCACTGCAAC CTTGAACCTC TGGGCTCAAG CAATCCTCCT
6951 GCCTCGGGCT CTTGAGTAGC TGGGACAACA GGTGTGCACC ACCACACCTG
7001 GCTAAATTTT TTTTTTTCT TTGTAGAGAT AGACTCTCAC TATGTTACCC
7051 AGGCTGGTCT TGAATTCCTG GGCTCATGTA ATCCTCTGTC TGCTTGAAAC
7101 TCCCAAAGTG CTGGGACTAT AGGCATAAGA CATCATGCCC GGTCGGGCAC
7151 AGTGGCTCAT GCCTGTAATC TCAGGACTTT GGGAGGCCGA GACGGGCGGA
7201 TCACCTGAGG TCGGGAGTTC GAGACCAGCC TGACCAACAT GGAGAAACCC
7251 CATCTCTACT AAAAAAATA ATACAAATTT AGCCGACGCT GGTGGCACAT
7301 GCCTGTAATC CCAGCTACTA GGGAGGCTGA GGCAGGAGAA TCGCTTGAAC
7351 CCGGGAGGCT TAGGTTGCGG TGAGCTGAGA TTGCAACATT GCACTCCAGC
7401 CTGGGCAACA AGAGCGAAAT TCCATCTCAA AAAAAAATAA AAAGAAAAAA
7451 AGAAAAAAGA CACCATGCCC TATAAGTAAA CTAGAATTAA GGTGACTCCT
7501 AAGGAAATAA ATAGTTTTTA ACTGTACGAA CTTTGGAAAG AATGGGGCCA
7551 ATTCTTTAAT TAAATGCAGC CTCCCTGTTT GTGGAGAAAG AAAAATTTTT
7601 CTTAACCTTA TTGCCCCATT TCTTTTCTCT TTTATTGAAT ATTTTTTAGT
7651 TTTAACTATA TGAATAACA CATAACGTTT ACCATCTTAA CCATTTTATG
7701 GTATACAGTA CAGTAGTGT CAGTACATTC ATACTGTTAT GCAATCAGTC
7751 TCCAGAAGTC TTCATGTTGC AAAGCTGAAA CTCTATACCC ATTAACCAAC

FIGURE 3B



7801	TGCCTGTTCC	TCCCTCCTCC	AACCCCTGGC	AATCACCTTT	TTTTTTTTGA
7851	GACGAAGTCT	CACTCTGTCA	CCCAGGCTAG	AGTGCGGTGG	CTCGATCTCG
7901	GCTCACTGCA	AGCTCCGCCT	CCCGGTTTCA	TGCCATTCTC	CTGCCTCAGT
7951	CTCCAAGCA	GCTGGGACTA	CAGGTGCCCG	TCACCACGCC	TGGCTAATTT
8001	TTTGATTTTT	TAGTAGAGAT	GGAGTTTCAT	CGTGTTAGCC	AGGCTGATCT
8051	CAAACTCCTG	GCCTCAAGTG	ATCCACCCGC	CTCGGCCTCC	CAAAGTGCTG
8101	GGACTACAGG	CGTGAGCCAC	TGTGCCTGGC	CAGGAAGTAG	ACTCTTGATA
8151	TTAGTTCTCT	CTGGTTGAAA	TGTTTTTAAA	AATGAAAGAG	AATGACTAAT
8201	AACAAAAACA	CAGAAAGTTA	TAAGGATTGA	TGAAGATGTG	GAGACTTTGA
8251	AACCCATGTA	TACCATTGGT	GGGAATGTGA	AACGACGCAG	CCCTGTGGAA
8301	AATGGTACAG	CAGTTACCTG	AGGTGAGGAG	TTTGAAACCA	ACCTGGCCAA
8351	CATGCAGAAA	CCCCGTCTCC	ATTAATGTA	CAAAAATTAG	CCAGGNNNNN
8401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN

FIGURE 3C

OIP E 301A
DEC 20 2002
PATENT & TRADEMARK

Docket No.: CL000685
Serial No.: 09/748,127
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN DRUG-METABOLIZING...

11701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12651	CCCTTCTCCT	CTTCTCTCCT	TCCTGTCTTC	CTCTCTTTCT	CTCTTTCTTT
12701	CTTGACAGGG	TCTCTCTTTG	TCTCCAGGC	TGGGGTGCAG	TGGTACAAGC
12751	ATAGCTCACA	GCAGCCTTGA	ACTCCTAGGC	TCAAGTGATC	CTCCACGTC
12801	AGCCTCTGA	GCAGCTGGGA	CAACGGGCTC	ATACCACCAT	GCCTGGCTAA
12851	TTTTTTAATT	TTTCGTAGAG	ACAAGGTCTT	GTTATATTGC	CCAGGCTGGT
12901	CTCAAACTCC	TGGGCTCAAA	TGCTTCTCTC	ACCTCAGCCT	CCCACGTGGC
12951	TGGGATTACA	GGCATGAGCC	ACTGCACGCC	ACTCAACACT	CCACAAATGT
13001	TGATGCCATT	ATGTTTTGTG	AACTAGTGTC	CCTGGCACCC	GAGACTTGTA
13051	CTCCACACTC	GAGGACCAAA	TAGACTGGGG	TGGGAAGGGG	TTTATAGTTT
13101	CATTATTATT	TCCCTCAGG	GCACGGAGGT	CTTCCCCCTC	CTTGGCTCCA
13151	TCCTGCATGA	CCCCAACATC	TTCAAGCACC	CAGAAGAGTT	CAACCCAGAC
13201	CGTTTTCTGG	ATGCAGATGG	ACGGTTCAGG	AAGCATGAGG	CGTTCCTGCC
13251	CTTCTCTTAA	GGTATCTGCT	GCAGCCCTGG	GTATCACAAG	CAGGTGCTGG
13301	CGAACTCCAG	GCATCTGTGC	CAGCTGGGGG	CACCTTCTCT	CACCTCTGGG
13351	TTACTGTTGG	CTCCTCCACC	TGCTGTTCCC	CCCGTGGGCC	TGGGTGTGAG
13401	GAATACTGAC	TCAGCCCTCT	CTCTCTCTCT	CTCTCACCA	GGAAGCGTG
13451	TCTGCCCTGG	AGAGGGCCTG	GCAAAAGCGG	AGCTCTTCCT	CTTCTTCACC
13501	ACCATCTTAC	AAGCCTTCTC	CCTGGAGAGC	CCGTGCCCGC	CGGTACACCC
13551	TGAGCCTCAA	GCCCACCGTC	AGTGGCCTTT	TCAACATTCC	CCCAGCCTTC
13601	CAGCTGCAAG	TCCGTCCCAC	TGACCTTCAC	TCCACCACGC	AGACCAGATG
13651	AAGGAAGGCA	ACTTGGAAAG	GTTGGGTGCC	CAGGACGGTG	CCTCCAGCCT
13701	CAACAGTGGG	CATGGACAGG	GTTAATGTCT	CCAGAGTGTA	CACTGCAGGC
13751	AGCCACATTT	ACACGCCTGC	AGTTGTTTTT	CGGAGTCTGT	CCCACGGCCC
13801	ACACGCTCAC	TTGACTCATG	CTGCTAAGAT	GCACAACCGC	ACACCCATAC
13851	ACAACACAAA	GGGCCACAAA	GCAACTGCTG	GGTAGCTTTT	CCACAGACAT
13901	AAATATAGTC	CATCTGCAAT	CACAAGCACA	TAGCCAGGTA	ACCCACCAAC
13951	TCCCTTGGAT	CTGCAGCCCA	CACGTGGGAG	TCTGGCTGTC	ACCTTCACAA
14001	GCCACAGAAA	CGGCCACACA	TGTTACAGC	TCACACGCCC	TCTCCATTCA
14051	TCGAACTTCT	CAGTGTCCCT	GTCCCTGGTG	CCTGGCACAG	GGAACAGCAT
14101	GCCCCCTCCG	GGGTCTATGC	ACCCAGAGAC	TGTCGCTGTC	TATGGCCCCA
14151	ACTCATGCTC	CCTCTCTTGG	CTACACCACT	CTCCCAGCCT	GTGACCACCG
14201	ATGTCCACAC	ACCCCAACCC	ACTTGTCCAC	ACAGCTACCC	ACGTACGACA
14251	TCGTCTCTGC	TCCCCAGAGT	ATCTTCCAC	TGAGACACGC	CGCCCCCACA
14301	GAGGCACAGT	CCCCAGCCAC	CTCTGCAACT	GCAGCCCTCA	GTCACCCCTT
14351	TTTAAGCACC	CTGATTCTAC	CAAAATGCAAA	CACATCTGGG	TCTGCGATTA
14401	TGCACAGAGA	CTTTGGACAT	ACGAGGACCC	TCAGACCGGA	GGAACACCTG
14451	CCCAACCCCA	ACACGTGCTT	ATGTAACCA	GTGGAAGCGG	GCCCCTGCTG
14501	CCCCCTCCCA	CACACATACA	CACTCACTGA	TCTACAGCCC	CTGTTCCGGC
14551	TCAGAGTCCC	CACTAGACCC	AGTGGAAAGG	GTTAGAGACC	AAGTAGGGGC
14601	CAGTTTCCAA	TTCAACCTGT	CAGGGAGTGA	GCCGGATCTG	ACGTTCTCTG
14651	TGACTTAAAG	GTCCGGCTTG	GGAATTAAG	TTTGTCTCTG	GCCTTTAGCC
14701	TACTGCGTGT	GTGACCCGTG	TCAGTCACTG	TGAGTAAGGG	GTGGGGACAG
14751	GGGAGTCCAC	CCCTCCCTTG	AGGCTGGGCG	GGAGCTGAAA	AACATGGCCA
14801	CCGCCACCC	TGGCTGTTGA	CATCAGGACC	AGATGTGGAG	CTGGGAGGAG
14851	GGGCAGGGCT	GGTGACGCCC	TGGGCTCAT	TTCCAAAAG	GGCCAAGGTG
14901	TCCGGCGGTG	GGAAAGTGGG	AAGGAGGGGG	TAACCCAAGC	TGGACTGTGG
14951	ACCTTGGGGG	CTTCTCAGC	CAGGGAGAGC	CTGAAGCCAA	CTAGATCCAG
15001	ACCCTAGAGA	CTCTTCAAAC	TTGAGTACAG	GAACTAGCTT	GCAACACAGA
15051	CTCTAAGCCC	ACTCCCATTT	CTTCCACCCT	TTTTCTCTTG	CCTCCCCTTC
15101	ACAAGGAAAC	CAGAGGCATT	TGTAATTTT	CTTTCTTTTT	TTTTTTTTTT
15151	TTTTTTTTGA	GACGGAGTCT	CACTCTGTCA	CCCAGGCTGG	AGTGCAGTGG
15201	TGTGATCTTG	GCTCACTGCA	GCCTCCGCCT	CCGGGTCAA	GCCATTCTCC
15251	TGCCTCAGCC	TCCCAAGTAG	CTGGGATTAC	AGGTGTGTGC	CACCACGCCC
15301	AGCTAATTTT	TGATTTTTTA	GTAAGATAGG	GGTTTACCA	TGTTGGCCAG
15351	GCTGGTCTCG	AACTCCTGAC	CTCAGATGAT	CTGCCAGTCT	CGGCCTCCCA
15401	AAATGCTGGG	ATTACAGGCG	TGAGTCGCTA	CTAGATAAAT	TTCTTATCTA
15451	GCAAAGAAGT	TGCAAAACAT	ACGCAAAAGT	AGAAAGATAC	AATGAGCCCC
15501	CAGGTGCCCA	TCACCCAGCC	TCATTTCAAT	AGTCATCAAC	TTTCTGCAGC
15551	TTTTACTTCA	TCTATATCCT	TTTCTGCCTC	TTTTTTTTTT	TTTTTATTTT

FIGURE 3D

DEC 20 2002
PATENT & TRADEMARK

Docket No.: CL000685
Serial No.: 09/748,127
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN DRUG-METABOLIZING...

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15601 GAGATAGGGT TTTGCTTTGT TGCCCAAGCT GGGGTGCAGT AGCATGATCT
15651 CATAGTTTAC TGGGGCTTCA GACTCCTAGG CTCAAGTGAT CCTCCCGCT
15701 CGGCCTCCAA GCAGCTGGGA CTACAGATGC GTGCCACCAC ACCCAGCTAA
15751 ATTTCTTATT TTTATTTTCT ATAGAGAAAG TCTCACTATA CAGCCCTGTG
15801 CTGGTCTCAA ATTCCAGGCC TCAAGAGTTT CCATCCCAGC CTCCCAAAGT
15851 GCTGGGATTA TAGGCGTGAG TCACTGCACC CTGCCCTAAT ATTTTATTTT
15901 TATCTATTGC TTTTATTTA CTTATTTATC TTTTATTTT GAGACAGAGT
15951 CTCACTCTGT GGGCCATGCT GGAGTGCACT GGCATCATCT CGGCTCACTG
16001 TAACCTCCGC CTCTTAGGTT CAAGCAGTTC TCCTGCCTTG ACCTCCCGAG
16051 TAGCTGGAAT TACAGGTGCC TGCCACCAAG CCTGGCTAAT TTTTATTTT
16101 GTAGTAGAGA TGGGGTTTTG CCATGTTGAC CAGGCTGGTC TCGAACTCCT
16151 GACCTCAGGT GATCTGCCCA CTTTGGCCTC CCAAAGTGCT GAGATTACTG
16201 GTATGAGCCA CCGTGCCTGG CCACCTATTG CTTTTTAAAG ATTATTTTIT
16251 TATTATTATT ATTTTITTTT TTGCAGATGG AGTTTCGCTA TTGTTGCCCA
16301 GGCTGGAGTG CAATGGCGTG ATCTCAGTCT ACCGCAACCT CCGCTCCCA
16351 GGTTCAGCG ATTCTCCTGC CTCAGCATCC CTAGTAGCTG GGATTACAGG
16401 CATGCACCAC CATGTCAGC TAATTTTGTA TTTTATAGTAG AGACGAGGTT
16451 TCTCCAGGTT GGTCAGGCTG GTCTCAAACCT CCAACCTCA GGTGATCCGC
16501 CCATCTCGGC CTCCCAAAGT GCTGGGATTA CAGGTGTGAG CCACCGCGCC
16551 TGGCCTTAAA GATTATTTTA AGGCAAATTA CAGAAAGCAA TTTAATGCAC
16601 ATTTCTGAGA GTTAAAGATA TTTTGGCCT TGACATTTTA TGAGGACAGT
16651 TTTCAACAT GCAGCAAAGT TGAGGGAATT GTACAAGGAA CACCTTGTGC
16701 ACTCCTGCCT CAGTCTCCCA AGCAGCTGGG ACTACAGGTG CCGCTACCA
16751 CGCCTGGCTA ATTTTGTGA TTTTATAGTAG AGATGGAGTT TCATCGTGTT
16801 AGCCAGGCTG ATCTCAAACCT CCTGGCCTCA AGTGATCCAC CCGCTCGGC
16851 CTCCCAAGTG CTGGGACTAC AGGCGTGAGC CACTGTGCCT GGCCAGGTAA
16901 GTAGACTCTT GATATTAGTT CTCTCTGGTT GAAATGTTTT TAAAAATGAA
16951 AGAGAATGAC TAATAACAAA AACACAGAAA GTTATAAGGA TTGATGAAGA
17001 TGTGGAGACT TTGAAACCCA TGTATACCAT TGGTGGGAAT GTGAAACGAC
17051 GCAGCCCTGT GGAATGGT ACAGCAGTTA CCTGAGGTCA GGAGTTTGAA
17101 ACCAACCTGG CCAACATGCA GAAACCCCGT CTCCATTAAA TGTACAAAAA
17151 TTAGCCAGGC ATGGTGGTGC GCACCTGTAA TCCAGCTAC TCGGGAGGCT
17201 GAGGCAGGAG AATTGCTTGA ACCCAGGAGG CGGAGGTTGC AGTGAGCCGA
17251 GATCGTGCCA CTGCACTCAG CCTGGGCAAC AAAGCAAGAC TCTGTCTCAA
17301 AAAAAAAAG TCTACTTCCC AACCTTCCCA AAAATTTATC TAAACCCCGT
17351 GACAAAACCT TAACCTGTGT TTCCGACCCC AGGCTTGGCT GTTCTGGACA
17401 TTTACTTCCC AAAGGCTGTG TTCTCTCAGC CCCTCTGCCT GGTTTCTTTC
17451 AGGAGGAACA AAACCCAGGC ACAGAATTCA CCAACAAGAA CATGCTGATG
17501 ACAGTCATTT ATTTGCTGTT TGCTGGGACG ATGACGGTCA GCACCACGGT
17551 CGGCTATACC CTCCTGCTCC TGATGAAATA CCCTCATGTC CAAAGTAAGA
17601 GCCTTTTCCA CTTGCCAGGC CTTGGGAACA GAAGTCAGGG TTCTAGGCTG
17651 AGCAAGGTGG CTCACGCCTA TAATCCCAGC ACTTTGGGAG GCTGAGGCGG
17701 GCTGATCACT TGAGAAATAG AGTTTAAAGAC CAGCCGGCCA ACACAGTGAA
17751 AC (SEQ ID NO:3)

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FEATURES:

Start:	1999	6349
Exon:	1999	2167
Intron:	2168	5236
Exon:	5237	5386
Intron:	5387	5919
Exon:	5920	6080
Intron:	6081	6166
Exon:	6167	6349
Intron:	6354	13542
Exon:	6354	6636
Intron:	6637	13087
Exon:	13088	13261
Intron:	13262	13441
Exon:	13442	13542
Intron:	13547	13648
Exon:	13547	13648
Stop:	13649	

SNPs:

DNA

Position	Major	Minor
2226	G	C A
2226	C	A G T
3081	A	T G C
3788	A	T
3979	T	C G
5056	T	C G
5213	T	G A C
5508	A	C T G
5857	C	G A T

FIGURE 3E



Docket No.: CL000685
Serial No.: 09/748,127
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN DRUG-METABOLIZING...

6385	C	T G
6813	C	T A
7853	C	T
12973	G	C T
12973	A	G T
13012	G	A C T
13072	A	T C G
13370	C	G
13682	C	T A
14631	C	T G

Context:

DNA
Position

2226 TGACAGGGGCCATGATGGAGACACCTTGGATCGAAGAGGTCACAGCACCTCCTCTTTCT
TCCTCCCTACCCCCAGCTGAGTAAGAAGTACGGACCGGTGTTCAACATCTACCTGGGACC
CTGGCGGCCTGTGGTGGTCCTGGTTGGGCAGGAGGCTGTGCGGGAGGCCCTGGGAGGTCA
GGCTGAGGAGTTCAGCGGCCGGGAACCGTAGCGATGCTGGAAGGGACTTTTGATGGCCA
TGGAAGTCAAGGGCTGCTAGGCCCTCCGCTCACAGCCTGCCACCACTTACTGGTGTGTG
[G,C,A]
CCTTTGCACATGGCTTAGTCCCTCTGTTGCCTCATCTGTCAAATGGAGTGATAACAGTGC
CCATCAGCCGGGTGCAGTGGCTAGTGCCTGAAATCCAACACTTTGGGAGGCGGAGGTGG
GTGGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAACCCCTGTCT
CTACTAAAAATATAAAATTAGCTGGGCATGGTGGTGCCTACCTGTAATCCAGATACTT
GGGAGGTTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGATGTTGCAGTGAACCAAGA

2226 TGACAGGGGCCATGATGGAGACACCTTGGATCGAAGAGGTCACAGCACCTCCTCTTTCT
TCCTCCCTACCCCCAGCTGAGTAAGAAGTACGGACCGGTGTTCAACATCTACCTGGGACC
CTGGCGGCCTGTGGTGGTCCTGGTTGGGCAGGAGGCTGTGCGGGAGGCCCTGGGAGGTCA
GGCTGAGGAGTTCAGCGGCCGGGAACCGTAGCGATGCTGGAAGGGACTTTTGATGGCCA
TGGAAGTCAAGGGCTGCTAGGCCCTCCGCTCACAGCCTGCCACCACTTACTGGTGTGTG
[C,A,Gst]

FIGURE 3F

DEC 2 0 2002
PATENT & TRADEMARK OFFICE

Docket No.: CL000685
Serial No.: 09/748,127
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN DRUG-METABOLIZING...

CCTTTGCACATGGCTTAGTCCCTCTGTTGCCTCATCTGTCAAATGGAGTGATAACAGTGCC
CCATCAGCCGGGTGCACTGGCTAGTGCCTGAAATCCCAACACTTTGGGAGGCGGAGGTGG
GTGGATCACTTGAAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTGTCT
CTACTAAAAATATAAAAAATAGCTGGGCATGGTGGTGCCTGTAATCCAGATACTT
GGGAGGTTGAGGCAGGAGAATCGCTTGAAACCCGGGAGGCAGATGTTGCAGTGAACCAAGA

3081 AAACAGTTCTCTGTATTACAACAGAAAGCAGGAGGCCCATGCTGGGTGCTGCCAGGAAC
CAGTAGTAATAAGACAGCACCGGTGCTGCTTCCCAGCGCACCTAGGCCAGTGGGGAAA
CAGACTCACCACACAGTCCCAGCCAGAGTGGTCAGGGCCAAGATGGGGAAGCACGGGGA
GAAAGGTGAGGTGGGATGGGAGGGGTGAGGCAAGAGGGGTGAGGCCAGGCTGAGGG
AAGCCCTGGGACTGTAGGAATTTAGAGGAGGTACCTGACCCGGCATGTTTGGTGAGGGAG
[A, T, G, C]
TTGAGGAAGTCTTCTGGAAGAGAGGCTGTGCGAGCTGAGACTCATAAGATGAGTGGGA
GGGTGTTCCAGGCAGAAAGACAGCACCTACAAAGCATGACTTTGAGAGAAGCATTTCAT
CCATTCAACTGATGAATTTTCAAGTGGGCACGCTGGCTCATGCCTGTAATCCAGCACT
TTGGAAGGCTGAATGGGAGGATGACTTGAGCCTAGGCATTTGTGACAAGCCTGGGCAAC
ATGGTGAGACCCTGCCTCCACAAAACAAACAAACAAACAAATCATTATACCTGGTAC

3788 ATCTAAAAATGAGAGGTACAGATTTGAGAGCAAAACAGGGCACAGGCATATGTACGAGG
GTAAAGAGGGAATCAGGGAAGGCTTCTCAGAGAAGGTGACATTTAAGCCGGGACATGAAG
GATGAACGAGTTAGTTACCAAGGATGGGATGGAAGGGGTGAGAGTGATGGAGGCAGAG
GGAAGTGCAGGATCATAGGCTAGACAGGGGATCCTGACGCCCTTGAGGAAGTGAGAGAA
GACCAGCGCAGTCGTAGTGGGTTAAGTAACAAAGCTGAGAAGCCAGGGAATCCCTGGTC
[A, T]
TGCAGGCTGTGAGTCACGTGAGTGTGTTGGGCTTTTGTCTTCTGGGAGCAGTCGA
TTTTAAGCAGGGAACAGCTGTATTGAGAGTTGGGAAGATCCTGTGGTGTCTGCCTGAAGG
GGATGAACTGAGGCTAGGAGCCAGGGTGATAGGGAGGATCCAGGGTGATGGGAGGC
TGGGAGGTCGCGGTGATGGACAGGGCTGGGGCCAGGGGATGGGAGGAAGGAGTAATT
GGGAGAGGCTGGGCTGTGGCCGAGGAATGGATGGTGGGCTGAAACAGGGAGGAGGAG

3979 ATCATAGGCCTAGACAGGGGATCCTGACGCCCTTGAGGAAGTGAGAGAAGACCAGCGCAG
TCGTAGTGGGTTAAGTAACAAAGCTGAGAAGCCAGGGAATCCCTGGTCATGCAGGGCCT
GTGAGTCACGTGAGTGTGTTGGGCTTTTGTCTTCTGGGAGCAGTCGATTTTAAGCAG
GGAAACAGCTGATTGAGAGTTGGGAAGATCCTGTGGTGTCTGCCTGAAGGGGATGAAACT
GGAGGCTAGGAGCCAGGGTGATAGGGAGGATCCAGGGTGATGGGAGGCTGGGAGGTCC
[T, C, G]
CGGTGATGGACAGGGCTGGGGCCAGGGGATGGGGAGGAAGGAGTAATTGGGAGAGCCT
GGGGCTCTGGCCGAGGAATGGATGGTGGGCTGAAACAGGGAGAGGAGATGCTTAGGCC
ACTTTGGAACACAGTAGGGCAAGGACAGGAGACACCAAGGGGAAGTGCCCAAGAGACCA
CGAAGGCTGGCATTTGGACAGGGAAGGTCTGTCTGAGCAGGTGTCTTGATAAGGGAGG
AAAATGGTGAGTTCATCTCTCTCTCTCTGTTCACCTCTAACTACATGGGGCACA

5056 AGTTTGATTATGCATTTATTGAGCACCTACTGAGTCTCATCCCTGGGCTAGGCTGGAAT
GGACTCAGATGGAGCCTGAAGAGTCCCTCAGGGAACCTCACTAGAAAGAAGGAGGAAT
CGGCCGGGCGGGTGGCTCAGCCTGTAAATCCCAACACTTTGGGAGGCTGAGGTGGGTGG
ATCACAAGGTGAGAGATCGAGACCATCCTGGCTAACACAGTGAACCCCATCTCTACTA
AAAATACAAAAAATGAGCCAGGCATGGTGGCGGGCGCTGTAGTCCAGCTACTCAGGAG
[T, C, G]
CTGAGGCAGGAGAATTGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGACGAGATCACGC
CACTGCACTCAGCCTGGGCAACAGAGCGAGATTCCTGTCTCAAAAAAAGAAAGAAA
GGAAGAAGGGGAATGGGGGAGAGGGGCGGTCCCTTTTGTAGTCTAGCCTTCTGCGCAG
GGGTTTTCTTCCAACGGGAGCGGTGGAGGCAGCTGAGGAAGTTTACCATGCTTGTCT
TGCGGACCTGGGCATGGGAAGCGAGAAGCGAGGAGCTGATCCAGCGGAGGCCCGGT

5213 CTTTGGGAGGCTGAGGTGGGTGGATCACAAGGTGAGGATCGAGACCATCCTGGCTAAC
ACAGTGAAACCCCATCTCTACTAAAAATACAAAAATGAGCCAGGCATGGTGGCGGGCGC
CTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGAACCCGGGAGGCAGA
GGTTGCAGTGAGACGAGATCACGCCACTGCACTCCAGCCTGGGCAACAGAGCGAGATTCC
GTCTCAAAAAAAGAAAGAAAGGAAGGGAATGGGGAGAGGGGCGGTCCCT
[T, G, A, C]
TTTGAGTCTAGCCTTCTGCGCAGGGGTTTTCTTCTCCAACGGGAGCGGTGGAGGCAGCT
GAGGAAGTTTACCATGCTTGTCTGCGGGACCTGGGCATGGGGAAGCGAGAAGGCGAGGA
GCTGATCCAGGCGGAGGCGCGGTGTCTGGTGGAGACATTCAGGGGACAGAAGGTGAGCA
TGGCGGGGTCAACCCAGGGTCTCAGCCGAGTGAAAGGGAAAACTCTCTACTGTGGCTG
GGGTGGCCCAACCCAGGTCTGGAATGGGCAGGAGGGAAGCCTTGAACCTAGGGCT

5508 TCCCTTTTGTAGTCTAGCCTTCTGCGCAGGGGTTTTCTTCTCCAACGGGAGCGGTGGAG
GCAGCTGAGGAAGTTTACCATGCTTGTCTGCGGGACCTGGGCATGGGGAAGCGAGAAGG
CGAGGAGCTGATCCAGGCGGAGGCGCGGTGTCTGGTGGAGACATTCAGGGGACAGAAGG
TCAGCATGGCGGGGTCAACCCAGGGTCTCAGCCGAGTGAAAGGGAAAACTCTCTACTG
TGGCTGGGGGTGGCCCCAACCCAGGTCTGGAATGGGCAGGAGGGGAAGCCTTGAACCT
[A, C, T, G]
GGGCTGGCCTGGGGTTCTGTCTACTGCCACCTTCTGTCTGTCTCCACTGTCTCTCGA
GGCTGTCAATGACATCTCTGTGTGTCTGTGTGTATCATCCATTCTTCTGGGTCTC
CATCTCTCTCTGTCTCTTTTCTTCTCTCTCTTCTCTATTTTGGGCCCTCAGT
CTATCTCTGTTTCTGTCTCCCTGTCTGTGTGATGGTCACTCTGTTTCTTCTCCCTGTCT
GTTTCTCTGTCCCTATCTGTCTGTATCTTCTTTCCTGTTTGTCTCTCCCTGCGCTG

FIGURE 3G

Serial No.: 09/748,127

Title: ISOLATED HUMAN DRUG-METABOLIZING...

CTGTCTCTCCGAGGCTGTCA TGACATCTCTCTGTGTCTCTGGTGCTATCATCCATTCT
TTCCTGGGCTCTCATCTCTCTCTGTCTCTTTCTTTCTCTCTCTTTCTCTATTTT
TGCGGGCTCAGTCTATCTCTGTTTCTGTCTCGCTGCTGTGTGATGGTCACTCTGTTCT
TCTCCCTGTCTGTTTCTCTGTCCCTATCTGCTGATCCTCTTTGCTGTTAGTCT
CTCCCTGCGCTGCCATCCATCTTCCCTGCTCCCTCTCTCTCTGCTGGGTCAAG
[C, G, A, T]

CCAACTCTCTCCCTCTGCTGGCTCCATCACAGCCTACCTCCCTGCCCCATTCCCCC
AGGAGCCCCATTCGATCCCTCCCTGCTGCTGGCCAGGCCACCTCCAACGTAGTCTGCTC
CCTCTCTTCTGGCTCCGCTTCTCTATGAGGATAAGGAGTTCCAGGCCGTGGTCCGGGC
AGCTGGTGGTACCTCTGCGGAGTCAGCTCCAGAGGGGTCAAGTGAGTGGGTGGGACCC
CTCTCCAAC TACCTTCCCTGAAGGTTCTGCCAAGGTC CATGAGA ACTAGCTGCCCTTC

GTGGGTGGGACCCCTCTCCAACCTACCTTCCCTGAAGGTTCTGCCAAGGTCCCATGAGAA
CTAGCTGCCCTTCTCCCCACAGACCTACGAGATGTTCTCTGTTTCTGCGGCCCTGCC
AGCCCCACAAGCAGCTCTCTCCACAGCTCAGACACTTGGCTGCCCTTACAGTCCGGCA
GGTGACAGCACCAGGGGAACCTGGATGCTTCCGGCCCCAGCTGACCTTGTCTGATGC
CTTCTGCTGAAGATGGCACAGGTGTGGGAAGGGTGCAGGGACCCCTCTGAATGGGC
[C, T, G]
TGGTGACCTGGCAGGTCCAGACCAGGTGTCCCTGGGGACCTCAATTGGGTTCTCTCTCT
TTCTCTCTCTGCATGTCTCTGTGAGTATGAGTGTCTCTGTGCATGTGTGTGCATCCCTTC
TCTGCACATCTGTGCTGCCCTTCTCAGGGCGTTGCTCTCACTGCCCTCCCCGCCCGAC
TCGGGCATTTGTGCGGGGTGTCTGTCTCTCAGCATCTCTCTCTTCTCCCTCCACC
TCGGCCCTTGTTGTCAGGCCCATGCCAGGGTCTACACCAAGAATCCCAAGGATCACT

ATCTGTGCTGGCCCTTTTCAGGGCGTTGCTCTCACTGCCTCTCCGCCCCGACCTGGGCA
TTTGTGCCGGGCTGTCTGCTCTCCAGCATCTCTCCTCTTTCTCCCTCCCACTCGGGCC
TTGTTGTCAGGCCCATGCCAGGGTCTACACAGCAATCCCAAGGATCACTTCATCCC
ATCCCTCGACGCTCCCCAGACTTTATGTAAATTCACAAATTTATGTAATTAGTGCA
TTTATTAGGAAGCCTTGAATATCAAGTTATGTTAATAAAGTCACCTTTAATTAATAT
[C, T, A]
AGAACAAATATTTCTTTCTTTTTTTCTTTCTTTTAAAGAGCAGGATCTCTTTC
TGTTGCCAGGCTAGAGTACAGTTGCAAAATCATAGCTCACTGCAACCTTGAACCTCTGG
GCTCAAGCAATCTCTGCCTCGGGCTCTGAGTAGCTGGGACAACAGGTTGCAACCACC
ACACCTGGCTAAATTTTTTTTTTTCTTTCTGTAGAGTAGACTCTCACTATGTTACCCAGG
CTGGTCTTGAATTCCTGGGCTCATGTAATCTCCTCTGTCCTTGAACCTCCAAAGGCTGTG

TCTTTAATTAAATGAGCCTCCCTGTTTGTGGAGAAAGAAAAATTTTTCTTAACCTATT
GCCCACTTTCTTTTCTCTTTATTGAATATTTTTAGTTTAACTATAGTAAAAACACA
TAACGTTTACCATCTTAACCAATTTAGGTATACAGACAGTAGTGTCAGTACATTCAT
ACTGTATGCAATCAGTCTCCAGAAGCTTCATGTGCAAGCTGAACTCTATACCAT
TAAACAAGTGCCTGTTCTCTCCCTCTCAACCCCTGGCAATCACCTTTTTTTTTTGAGA
[C,T]
GAAGTCTCACTCTGTCAACCAGGCTAGAGTGCGGTGGCTCGATCTCGGCTCACTGCAAGC
TCCGCTCCCGGGTTCATGCCATTCTCTGCCTCAGTCTCCAAGCAGCTGGGACTACAG
GTGCGCGTCAACCAAGCCTGGCTAATTTTTGTATTTTTAGTAGAGTAGGAGTTTCATCGT
GTAGCCAGGCTGATCTCAAACTCTGGCCTCAAGTGATCCACCGCCTCGGCCTCCCAA
AGTGTCTGGGACTACAGGCGTGAGCCACTGTGCCGTGCCAGGAAGTAGACTCTTGATATTA

CTGTCTCTCTCTTTCTCTCTTTCTTTCTTGACAGGGTCTCTTTGTCTCCGAGGCTG
GGGTGCAGTGGTACAGCATAGCTCACAGCAGCCTTGAACCTCTAGGCTCAAGTGATCCT
CCCAGCTCAGCCTCCTGAGCAGCTGGGACCAAGGGCTCATACCAACATGCCTGGCTAATT
TTTAAATTTTTCGTAGAGACAAGTCTTTGTATATTGCCAGGCTGGTCTCAAACTCTG
GGCTCAAATGCTTCTCTACCTCAGCCTCCACGTGGCTGGGATTACAGGATCAGGCCAC
[G, C, T]
GCAGCGCACTCAACACTCCACAAATGTTGATGCCATTATGTTTGTGAACTAGTGCCCT
GGCAGCCGAGACTTGTA CTCCACTCGAGGACCAAA TAGACTGGGGTGGGAAGGGGTTT
ATAGTTTTCATTATTTATTTCCCTCAGGGCAGGAGGTCCTCCCTCTTGGCTCCATCC
TGCA TGACCCCAACATCTTCAAGCACAAGAAGTTCAACCAGACCCGTTTCTGGATG
CAGATGGACGGTT CAGGAAGCATGAGGC GTTCTGCCCTTCTCTAGGTATCTGCTGCA

FIGURE 3H

DEC 20 2002
PATENT & TRADEMARK

Docket No.: CL000685
Serial No.: 09/748,127
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN DRUG-METABOLIZING...

12973 CTGTCTTCTCTCTTTCTCTCTTTCTTTCTTGACAGGGTCTCTCTTTGTCTCCAGGCTG
GGGTGCAGTGGTACAAGCATAGCTCACAGCAGCCTTGAACCTCTAGGCTCAAGTGATCCT
CCCACGTGAGCCTCTGAGCAGCTGGGACAACGGGCTCATACCACCATGCCTGGCTAATT
TTTTAATTTTTCTGAGAGACAAGGTCTTGTATATTGCCAGGCTGGTCTCAAACCTCTG
GGCTCAAATGCTTCTCTCACCTCAGCCTCCCACGTGGCTGGGATTACAGGCATGAGCCAC
[A, G, T]
GCACGCCACTCAACACTCCACAAATGTTGATGCCATTATGTTTTGTGAAGTGTCTCCCT
GGCACCAGAGCTTGTACTCCACACTCGAGGACCAATAGACTGGGGTGGGAAGGGGTTT
ATAGTTTCATTATTATTTCCCTCAGGGCACGGAGGTCTTCCCTCTCTGGCTCCATCC
TGCATGACCCCAACATCTTCAAGCACCAGAAGAGTTCAACCCAGACCGTTTCTGGATG
CAGATGGACGGTTCAGGAAGCATGAGGCGTTCTGCCCTTCTCTAGGTATCTGCTGCA

13012 CTCTCTTTGTCTCCAGGCTGGGGTGCAGTGGTACAAGCATAGCTCACAGCAGCCTTGAA
CTCCTAGGCTCAAGTGATCCTCCCACGTGAGCCTCTGAGCAGCTGGGACAACGGGCTCA
TACCACCATGCCTGGCTAATTTTTAATTTTTCTGAGAGACAAGGTCTTGTATATTGCC
CAGGCTGGTCTCAAACCTCTGGGCTCAAATGCTTCTCTACCTCAGCCTCCCACGTGGCT
GGGATTACAGGCATGAGCCACTGCACGCCACTCAACACTCCACAAATGTTGATGCCATTA
[G, A, C, S, T]
GTTTTGTGAAGTGTCTCCCTGGCACCAGAGCTTGTACTCCACACTCGAGGACCAATA
GACTGGGGTGGGAAGGGGTTATAGTTTCATTATTATTTCCCTCAGGGCACGGAGGTCT
TCCCCCTCTTGGCTCCATCTGCTGACCCCAACATCTTCAAGCACCAGAAGAGTTCA
ACCCAGACCGTTTCTGGATGCAGATGGACGGTTCAGGAAGCATGAGGCGTTCTGCCCT
TCTCCTTAGGTATCTGCTGCAGCCTGGGTATCACAAGCAGGTGCTGGCGAACTCCAGGC

13072 CTCCTAGGCTCAAGTGATCCTCCCACGTGAGCCTCTGAGCAGCTGGGACAACGGGCTCA
TACCACCATGCCTGGCTAATTTTTAATTTTTCTGAGAGACAAGGTCTTGTATATTGCC
CAGGCTGGTCTCAAACCTCTGGGCTCAAATGCTTCTCTACCTCAGCCTCCCACGTGGCT
GGGATTACAGGCATGAGCCACTGCACGCCACTCAACACTCCACAAATGTTGATGCCATTA
TGTTTTGTGAAGTGTCTCCCTGGCACCAGAGCTTGTACTCCACACTCGAGGACCAAT
[A, T, C, S, G]
GACTGGGGTGGGAAGGGGTTATAGTTTCATTATTATTTCCCTCAGGGCACGGAGGTCT
TCCCCCTCTTGGCTCCATCTGCTGACCCCAACATCTTCAAGCACCAGAAGAGTTCA
ACCCAGACCGTTTCTGGATGCAGATGGACGGTTCAGGAAGCATGAGGCGTTCTGCCCT
TCTCCTTAGGTATCTGCTGCAGCCTGGGTATCACAAGCAGGTGCTGGCGAACTCCAGGC
ATCTGTGCCAGCTGGGGGCACCTTCTGCACCCTGGGCTTACTGTTGGCTCCTCCACCTG

13370 ATAGACTGGGGTGGGAAGGGGTTTATAGTTTCATTATTATTTCCCTCAGGGCACGGAGG
TCTTCCCCCTCTTGGCTCCATCTGCTGACCCCAACATCTTCAAGCACCAGAAGAGT
TCAACCCAGACCGTTTCTGGATGCAGATGGACGGTTCAGGAAGCATGAGGCGTTCTGCTG
CCTTCTCCTTAGGTATCTGCTGCAGCCCTGGGTATCACAAGCAGGTGCTGGCGAACTCCA
GGCATCTGTGCCAGCTGGGGGCACCTTCTGCACCCTGGGCTTACTGTTGGCTCCTCCAC
[C, G]
TGCTGTTCCCCCGTGGGCTGGGTGTGAGGAATACTGACTCAGCCCTCTCTCTCTCTCT
CTCCTCACCAGGGAAGCGTGTCTGCCTTGGAGAGGGCTGGCAAAAGCGGAGCTCTTCTCT
CTTCTTCAACACCATCTTCAAGCCTTCTCCCTGGAGAGCCGTGCCCGCCGGTACACCC
TGAGCCTCAAGCCCACCGTCAAGTGGCTTTTCAACATTCCCCAGCCTTCCAGCTGCAAG
TCCGTCCCCTGACCTTCACTCCACCACGAGACAGATGAAGGAAGGCAACTTGAAGT

13682 CCGTGGGCTGGGTGTGAGGAATACTGACTCAGCCCTCTCTCTCTCTCTCTCTCACCAG
GGAAGCGTGTCTGCCTTGGAGAGGGCTGGCAAAAGCGGAGCTCTTCTCTTCTTCAACA
CCATCCTACAAGCCTTCTCCCTGGAGAGCCGTGCCCGCCGGTACACCTGAGCCTCAAG
CCCACCGTCAAGTGGCTTTTCAACATTCCCCAGCCTTCCAGCTGCAAGTCCGTCCACT
GACCTTCACTCCACCACGAGACAGATGAAGGAAGGCAACTTGAAGTGGTGGGTGCC
[C, T, A]
GGACGGTGCCTCCAGCCTCAACAGTGGGATGGACAGGGTTAATGTCTCCAGAGTGTACA
CTGAGGCAGCCACATTTACACGCTGAGTTGTTTTCCGGAGTCTGTCCCACGGCCAC
ACGCTCACTTGAATGCTGCTAAGATGCACAACCGCACCCATACACAATAAAGG
GCCACAAAGCAACTGCTGGGTAGCTTTCCACAGACATAAATATAGTCCATCTGCAATCA
CAAGCACATAGCCAGGTAACCCACCAACTCCCCTGATCTGCAGCCACACGTGGGAGTC

FIGURE 3I



Docket No.: CL000685
Serial No.: 09/748,127
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN DRUG-METABOLIZING...

14631

GCAGCCCTCAGTCACCCCTTTTAAAGCACCTGATTCTACCAAATGCAAACACATCTGGG
TCTGCGATTATGCACAGAGACTTTGGACATACGAGGACCCTCAGACCGGAGGAACACCTG
CCCAACCCCAACACGTGCTTATGTAACCACGTGGAAAGCGGCCCTGCTGCCCTCCACA
CACACATACACACTCACTGATCTACAGCCCTGTTGCGCGTCAGAGTCCCCACTAGACCC
AGTGGAAGGGGTTAGAGACCAAGTAGGGGCCAGTTTCCAATTCACCTGTCAGGGAGTGA
[C,T,G]
CCGGATCTGACGTTCTTGTGACTTAAGGGTCCGGCTTGGGAATTAAGTTTGTCTGG
CCTTTAGCCTACTGCGTGTGTGACCCGTGTCAGTCACTGTGAGTAAGGGGTGGGACAGG
GGAGTCCACCCCTCCCCTGAGGCTGGGCGGGAGCTGAAAAACATGGCCACCGCCACCCT
GGCTGTTGACATCAGGACCAGATGTGGAGCTGGGAGGAGGGCAGGGCTGGTGACGCCCT
GGGCCTCATTTCAAAAAGGGCCAAGGTGTCCGGCGTGGGAAGTGGCAAGGAGGGGT

Chromosomal Map Position

ePCR to dbSTS			
Site (bases)	Marker	Chr.	Organism
15155..15288	stSG46708	19	Homo sapiens

FIGURE 3J